

10/1/05

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 75%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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ALIGNMENTS

RESULT 1
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 ; Sequence 305, Application US/10131827
 ; Publication No. US20040009479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlgemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodward, Robert
 ; APPLICANT: Ly, Ngoc
 ; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
 ; FILE REFERENCE: 506612000120
 ; CURRENT APPLICATION NUMBER: US/10/131,827
 ; CURRENT FILING DATE: 2002-09-06
 ; PRIOR APPLICATION NUMBER: US 10/006,290
 ; PRIOR FILING DATE: 2001-10-22
 ; PRIOR APPLICATION NUMBER: US 60/296,764
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 9090
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 305
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-131-827-305

Query Match 5.7%; Score 50; DB 1; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 ACATCCCTTGAGTAGCTGAGCCGCTTAACTCATCTGTCCTGC 579
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 DB 1 ACATCCCTTGAGTAGCTGAGCCGCTTAACTCATCTGTCCTGC 50

RESULT 2
 US-10-131-827-1951
 ; Sequence 1951, Application US/10131827
 ; Publication No. US20040009479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wohlgemuth, Jay
 ; APPLICANT: Fry, Kirk
 ; APPLICANT: Woodward, Robert
 ; APPLICANT: Ly, Ngoc
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
 ; FILE REFERENCE: 506612000120
 ; CURRENT APPLICATION NUMBER: US/10/131,827

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C 321	19	2.2	25	1	US-10-700-816-11	Sequence 11, Appl	C 394	17.2	2.0	22	1	US-09-903-943-7	Sequence 7, Appl
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115	20	2.3	20	1	US-10-633-843-14	Sequence 14, Appl	c 188	20	2.3	20	1	US-10-672-866-20	Sequence 20, Appl
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117	20	2.3	20	1	US-10-633-843-16	Sequence 16, Appl	c 190	20	2.3	20	1	US-10-672-866-22	Sequence 22, Appl
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119	20	2.3	20	1	US-10-633-843-18	Sequence 18, Appl	c 192	20	2.3	20	1	US-10-672-866-24	Sequence 24, Appl
120	20	2.3	20	1	US-10-633-843-19	Sequence 19, Appl	c 193	20	2.3	20	1	US-10-672-866-25	Sequence 25, Appl
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123	20	2.3	20	1	US-10-633-843-22	Sequence 22, Appl	c 196	20	2.3	20	1	US-10-672-866-28	Sequence 28, Appl
124	20	2.3	20	1	US-10-633-843-23	Sequence 23, Appl	c 197	20	2.3	20	1	US-10-672-866-29	Sequence 29, Appl
125	20	2.3	20	1	US-10-633-843-24	Sequence 24, Appl	c 198	20	2.3	20	1	US-10-672-866-30	Sequence 30, Appl
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128	20	2.3	20	1	US-10-633-843-27	Sequence 27, Appl	c 201	20	2.3	20	1	US-10-672-866-33	Sequence 33, Appl
129	20	2.3	20	1	US-10-633-843-28	Sequence 28, Appl	c 202	20	2.3	20	1	US-10-672-866-34	Sequence 34, Appl
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131	20	2.3	20	1	US-10-633-843-30	Sequence 30, Appl	c 204	20	2.3	20	1	US-10-672-866-36	Sequence 36, Appl
132	20	2.3	20	1	US-10-633-843-31	Sequence 31, Appl	c 205	20	2.3	20	1	US-10-672-866-37	Sequence 37, Appl
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163	20	2.3	20	1	US-10-633-843-62	Sequence 62, Appl	c 236	20	2.3	20	1	US-10-672-866-68	Sequence 68, Appl
164	20	2.3	20	1	US-10-633-843-63	Sequence 63, Appl	c 237	20	2.3	20	1	US-10-672-866-69	Sequence 69, Appl
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OM nucleic - nucleic search, using sw model

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Searched: 633 seqs, 13433 residues

Total number of hits satisfying chosen parameters: 1266

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 637 summaries

Database : pubdb.*

.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	48	5.5	48	1	Sequence 7, Appl
5	46.4	5.3	48	1	US-10-301-516-28
6	46.4	5.3	48	1	Sequence 28, Appl
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8	42	4.8	42	1	Sequence 8, Appl
9	42	4.8	42	1	US-10-859-321-11
10	42	4.8	42	1	Sequence 11, Appl
11	42	4.8	42	1	US-10-912-440-11
12	41	4.7	41	1	Sequence 73, Appl
13	41	4.7	41	1	US-10-912-440-73
14	41	4.7	41	1	Sequence 12, Appl
15	41	4.7	41	1	US-10-859-321-12
16	35	4.0	35	1	Sequence 74, Appl
17	35	4.0	35	1	Sequence 12, Appl
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25	25	2.9	25	1	US-10-894-721-3
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87	23	2.6	23	1	US-10-487-091-6	Sequence 6, Appli
88	22.6	2.6	30	1	US-09-918-421-7	Sequence 7, Appli
89	22.4	2.6	25	1	US-10-719-900-61538	Sequence 61538, A
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106	20.2	2.3	25	1	US-10-719-900-967669	Sequence 967669, A

Published - Applications - NA

399	13.4	1.5	16	1	ADJ92751	Bacillus cereus sp	C 472	12.8	1.5	17	1	AAF06352	Hammerhead ribozym
C 400	13.4	1.5	17	1	AAJ74883	Mouse flt-1 VEGF r	C 473	12.8	1.5	17	1	AAF04741	Hammerhead ribozym
401	13.4	1.5	17	1	AAJ71523	Human KDR VEGF rec	474	12.8	1.5	17	1	AAF05354	Hammerhead ribozym
C 402	13.4	1.5	17	1	AAJ71528	Human KDR VEGF rec	C 475	12.8	1.5	17	1	AAF06353	Hammerhead ribozym
C 403	13.4	1.5	17	1	AAJ74882	Mouse flt-1 VEGF r	C 476	12.8	1.5	17	1	ABK01327	Human NOGO Inozyme
C 404	13.4	1.5	17	1	AAJ96546	Potato citrate syn	C 477	12.8	1.5	17	1	ABK02166	Human NOGO DNazyme
C 405	13.4	1.5	17	1	AAJ965385	Hammerhead ribozym	C 478	12.8	1.5	17	1	ABA78805	APC mutation corr
C 406	13.4	1.5	17	1	ABK00398	Human NOGO Hammerh	C 479	12.8	1.5	17	1	ABA80972	LDLR mutation corr
C 407	13.4	1.5	17	1	ABK80441	MSH2 mutation corr	480	12.8	1.5	17	1	ABA78806	APC mutation corr
C 408	13.4	1.5	17	1	ABA80440	MSH2 mutation corr	481	12.8	1.5	17	1	ABA80973	LDLR mutation corr
C 409	13.4	1.5	17	1	ABT38905	Tumour suppression	C 482	12.8	1.5	17	1	ABA77178	Adenosine deaminas
410	13.4	1.5	17	1	ABT38165	Tumour suppression	483	12.8	1.5	17	1	ABT77177	Adenosine deaminas
411	13.4	1.5	17	1	ABT35779	Tumour suppression	C 484	12.8	1.5	17	1	ABL54647	Haemorrhagic Esche
C 412	13.4	1.5	17	1	ABT34906	Tumour suppression	C 485	12.8	1.5	17	1	ABL51265	Human p53AlPI asso
C 413	13.4	1.5	17	1	ACB64073	HCV minus strand D	486	12.8	1.5	17	1	ABN01599	Human GDMPLP-1 17-m
C 414	13.4	1.5	17	1	ACB60389	HCV DNazyme substr	C 487	12.8	1.5	17	1	ABN07776	Human GDMPLP-1 17-m
415	13.4	1.5	17	1	ACD58596	HCV DNazyme substr	C 488	12.8	1.5	17	1	ABN10222	Human GDMPLP-1 17-m
416	13.4	1.5	17	1	ACD62280	HCV minus strand D	489	12.8	1.5	17	1	ABN01598	Human GDMPLP-1 17-m
417	13.4	1.5	17	1	ADB44863	Tumour suppression	490	12.8	1.5	17	1	ABN08969	Human GDMPLP-1 17-m
C 418	13.4	1.5	17	1	ADJ50752	Human tumour suppr	491	12.8	1.5	17	1	ABN02717	Human GDMPLP-1 17-m
C 419	13.4	1.5	17	1	ADJ50925	Human PTGDR substr	492	12.8	1.5	17	1	ABN07230	Human GDMPLP-1 17-m
C 420	13.4	1.5	17	1	ADJ84553	HCV DNazyme substr	C 493	12.8	1.5	17	1	ABN07990	Human GDMPLP-1 17-m
421	13.4	1.5	17	1	ADJ85510	HCV DNazyme substr	C 494	12.8	1.5	17	1	ABN07989	Human GDMPLP-1 17-m
422	13	1.5	13	1	AAJ88558	Anti-SOD-1 295 cod	C 495	12.8	1.5	17	1	ABN08168	Human GDMPLP-1 17-m
C 423	13	1.5	13	1	AAJ88562	Anti-SOD-1 429 cod	C 496	12.8	1.5	17	1	ABN10221	Human GDMPLP-1 17-m
C 424	13	1.5	13	1	AAJ88560	Anti-SOD-1 359 cod	C 497	12.8	1.5	17	1	ABN07775	Human GDMPLP-1 17-m
425	13	1.5	13	1	AAJ88556	Anti-SOD-1 186 cod	498	12.8	1.5	17	1	ABN08167	Human GDMPLP-1 17-m
C 426	13	1.5	13	1	ABF54653	Oligonucleotide SE	499	12.8	1.5	17	1	ABN08967	Human GDMPLP-1 17-m
C 427	13	1.5	13	1	ABF56543	Oligonucleotide SE	500	12.8	1.5	17	1	ABN02716	Human GDMPLP-1 17-m
C 428	13	1.5	13	1	ABH01040	Oligonucleotide SE	501	12.8	1.5	17	1	ABN07229	Human GDMPLP-1 17-m
C 429	13	1.5	13	1	ABH01041	Oligonucleotide SE	C 502	12.8	1.5	17	1	ABN07229	Human GDMPLP-1 17-m
C 430	13	1.5	13	1	ABF54652	Oligonucleotide SE	C 503	12.8	1.5	17	1	ABN07229	Human GDMPLP-1 17-m
C 431	13	1.5	13	1	ABF56542	Oligonucleotide SE	C 504	12.8	1.5	17	1	ABN07229	Human GDMPLP-1 17-m
C 432	13	1.5	13	1	ABF56542	Oligonucleotide SE	C 505	12.8	1.5	17	1	ABN07229	Human GDMPLP-1 17-m
433	13	1.5	13	1	AAJ34052	Eosinophil peroxid	506	12.8	1.5	17	1	ABV79551	Human HTPL scannin
C 434	13	1.5	15	1	AAJ20174	Human eosinophil p	C 507	12.8	1.5	17	1	ABV79527	Human HTPL scannin
435	13	1.5	15	1	AAJ70268	Human DRD2 allele	508	12.8	1.5	17	1	ABV79550	Human HTPL scannin
436	13	1.5	15	1	AAJ29568	Human eosinophil p	C 509	12.8	1.5	17	1	ABV91351	Human POSHL1 scann
C 437	13	1.5	15	1	ABD19123	Human eosinophil p	C 510	12.8	1.5	17	1	ABV91350	Human POSHL1 scann
C 438	13	1.5	15	1	ADH17043	Tagman probe used	C 511	12.8	1.5	17	1	ABL31225	Human HLA genotypl
C 439	13	1.5	16	1	ADJ56222	Aspergillus oryzae	C 512	12.8	1.5	17	1	ABK56978	Human CLCA1 gene e
440	13	1.5	17	1	AAJ69153	Human flt1 VEGF r	C 513	12.8	1.5	17	1	ACN11597	WNV minus strand I
C 441	13	1.5	17	1	ABK00483	Human NOGO Hammerh	C 514	12.8	1.5	17	1	ACN05534	WNV minus strand I
C 442	13	1.5	17	1	ABK00485	Human NOGO Hammerh	C 515	12.8	1.5	17	1	ACN11447	WNV minus strand I
C 443	13	1.5	17	1	ACA07852	NFKB sub-unit modu	C 516	12.8	1.5	17	1	ACN02441	WNV inozyme substr
444	13	1.5	17	1	ACC67156	NFKB sub-unit modu	C 517	12.8	1.5	17	1	ACN11448	WNV minus strand I
C 445	13	1.5	17	1	ADL51944	Human PTGDR substr	C 518	12.8	1.5	17	1	ACN10975	WNV minus strand I
C 446	13	1.5	17	1	ADL51944	Human PTGDR substr	C 519	12.8	1.5	17	1	ACN10975	WNV minus strand I
C 447	13	1.5	17	1	ADL51945	Human PTGDR substr	C 520	12.8	1.5	17	1	ACN08680	WNV minus strand H
C 448	13	1.5	17	1	ADL51945	Human PTGDR substr	C 521	12.8	1.5	17	1	ACN12972	WNV minus strand Z
449	12.8	1.5	16	1	AAJ68370	Human IRRR oligonu	522	12.8	1.5	17	1	ACN01916	WNV inozyme substr
450	12.8	1.5	16	1	ADJ53301	Target molecule de	523	12.8	1.5	17	1	ACN13888	WNV minus strand D
451	12.8	1.5	16	1	ADO43601	Mutant DNA fragmen	524	12.8	1.5	17	1	ACN02360	WNV inozyme substr
C 452	12.8	1.5	17	1	AAQ47893	SSP for flavonoid-	525	12.8	1.5	17	1	ACN06009	WNV Amberzyme subs
C 453	12.8	1.5	17	1	AAJ72611	Mouse flk-1 VEGF r	C 526	12.8	1.5	17	1	ACN11598	WNV minus strand I
454	12.8	1.5	17	1	AAJ75366	Mouse flt-1 VEGF r	527	12.8	1.5	17	1	ACN12158	WNV minus strand I
C 455	12.8	1.5	17	1	AAJ69933	Human flt1 VEGF r	528	12.8	1.5	17	1	ACN05025	WNV DNazyme substr
C 456	12.8	1.5	17	1	AAJ74524	Mouse flt-1 VEGF r	529	12.8	1.5	17	1	ACN06205	WNV Amberzyme subs
C 457	12.8	1.5	17	1	AAJ76334	Human fibronectin	C 530	12.8	1.5	17	1	ABT35891	Tumour suppression
C 458	12.8	1.5	17	1	AAJ97938	Human EGF-R target	C 531	12.8	1.5	17	1	ABT39802	Tumour suppression
C 459	12.8	1.5	17	1	AAJ96466	Potato citrate syn	532	12.8	1.5	17	1	ABT35521	Tumour suppression
C 460	12.8	1.5	17	1	AAJ49098	rb gene antisense	C 533	12.8	1.5	17	1	ABT38438	Tumour suppression
461	12.8	1.5	17	1	AAJ20557	Integrin alpha 6 s	C 534	12.8	1.5	17	1	ABT38549	Tumour suppression
C 462	12.8	1.5	17	1	AAJ21390	Integrin alpha 6 s	535	12.8	1.5	17	1	ABT39947	Tumour suppression
C 463	12.8	1.5	17	1	AAJ21391	Integrin alpha 6 s	C 536	12.8	1.5	17	1	ACA08213	NFKB sub-unit modu
464	12.8	1.5	17	1	AAJ54136	Human fibronectin	537	12.8	1.5	17	1	ADB00031	Human MD23 scannin
465	12.8	1.5	17	1	AAJ33580	Low adenosine anti	538	12.8	1.5	17	1	ADB00030	Human MD23 scannin
466	12.8	1.5	17	1	AAJ297540	HIV-1 protease gen	539	12.8	1.5	17	1	ADB03681	Human MD27 scannin
467	12.8	1.5	17	1	AAJ297701	HIV-1 protease gen	540	12.8	1.5	17	1	ADB03683	Human MD27 scannin
C 468	12.8	1.5	17	1	AAJ36411	Human genomic SNP	C 541	12.8	1.5	17	1	ABZ60096	Human K-Ras DNazym
469	12.8	1.5	17	1	AAJ19702	Human fibronectin	C 542	12.8	1.5	17	1	ABZ60986	Human K-Ras DNazym
470	12.8	1.5	17	1	AAJ04934	Hammerhead ribozym	543	12.8	1.5	17	1	ABZ61461	Human H-Ras DNazym
C 471	12.8	1.5	17	1	AAJ04293	Hammerhead ribozym	544	12.8	1.5	17	1	ACD51716	HBV inozyme substr

C 253	16	1.8	17	1	AAF91027	Human multi drug r
C 254	16	1.8	17	1	ADI50808	Human tumour suppressor
C 255	16	1.8	17	1	ADI50799	Human tumour suppressor
C 256	16	1.8	18	1	ABK41012	Human obesity-asso
C 257	16	1.8	19	1	AA150752	PAL/alpha-tubulin-
C 258	16	1.8	19	1	ADM83390	Coffea arabica PAL
C 259	15.8	1.8	20	1	AA159235	Anticense oligonuc
C 260	15.8	1.8	20	1	AAV85741	LRP5 exon primer E
C 261	15.8	1.8	20	1	ACC44079	Oligo ISIS 124670
C 262	15.8	1.8	20	1	ADL59647	Human ESM-1 antise
C 263	15.8	1.8	20	1	ADL59286	Human ESM-1 antise
C 264	15.8	1.8	21	1	AAV72769	Corn kernel oil co
C 265	15.8	1.8	21	1	ABS98130	Human multdrug re
C 266	15.6	1.8	17	1	ACF62527	Cancer based on CY
C 267	15.6	1.8	17	1	ADB21198	MRP1 based cancer
C 268	15.6	1.8	17	1	ADB88277	Human UGT1A1 varia
C 269	15.6	1.8	17	1	ADB97270	Human MDR1 variant
C 270	15.6	1.8	17	1	ADB92461	Human MDR1 variant
C 271	15.4	1.8	17	1	AAF03382	Hammerhead ribozym
C 272	15.4	1.8	17	1	AAF03383	Hammerhead ribozym
C 273	15.4	1.8	20	1	ADI81744	Human protein kina
C 274	15.4	1.8	20	1	ADI81684	Human protein kina
C 275	15.2	1.7	20	1	AAK08640	Primer for amplif
C 276	15.2	1.7	20	1	AAK33188	Human STAT3 phosph
C 277	15.2	1.7	20	1	AAH57024	Human oestrogen re
C 278	15.2	1.7	20	1	AAQ96805	Human STAT3 antise
C 279	15.2	1.7	20	1	ABQ99746	cuZnSOD primer #2
C 280	15.2	1.7	20	1	ABZ24780	Deoxyuridine monop
C 281	15.2	1.7	20	1	ACF39665	MHC class II trans
C 282	15.2	1.7	20	1	ADB99942	Vitamin D nuclear
C 283	15.2	1.7	20	1	ADF17531	Rhodotorula glutin
C 284	15.2	1.7	20	1	ABZ90760	Human oligonucleot
C 285	15.2	1.7	20	1	ABZ90984	Human oligonucleot
C 286	15.2	1.7	20	1	ABD26990	H93087-derived oli
C 287	15.2	1.7	20	1	ABD27214	AA180912-derived o
C 288	15.2	1.7	20	1	ADL59322	Human ESM-1 antise
C 289	15.2	1.7	20	1	ADL59256	Human ESM-1 antise
C 290	15.2	1.7	20	1	ADP11305	Set 1 right PCR pr
C 291	15.2	1.7	20	1	ADK21489	Acyl-coenzyme A sy
C 292	15.2	1.7	20	1	ADR70258	Human apoptosis-sp
C 293	15	1.7	15	1	AAV71205	Sequence of probe
C 294	15	1.7	15	1	AAQ61567	Human SOD probe.
C 295	15	1.7	15	1	ADQ36006	Wild type DNA frag
C 296	15	1.7	15	1	ADQ36006	Wild type DNA frag
C 297	15	1.7	17	1	AAH21293	Human MDR-1 allele
C 298	15	1.7	17	1	AAH21293	Human MDR-1 allele
C 299	15	1.7	17	1	AAV91028	Human multi drug r
C 300	15	1.7	17	1	ABT38676	Tumour suppression
C 301	15	1.7	17	1	ACF62526	Cancer based on CY
C 302	15	1.7	17	1	ADB21197	MRP1 based cancer
C 303	15	1.7	17	1	ADB88286	Human UGT1A1 varia
C 304	15	1.7	17	1	ADB97269	Human MDR1 variant
C 305	15	1.7	17	1	ADB92460	Human MDR1 variant
C 306	15	1.7	20	1	AAV13337	Anticense primer E
C 307	14.8	1.7	19	1	AAV72612	Glucose-6-phosphat
C 308	14.8	1.7	19	1	AAAB2988	cdk6 ribozyme bind
C 309	14.8	1.7	19	1	AAH58150	Cell-cycle depende
C 310	14.8	1.7	19	1	ADH01862	Protein tyrosine p
C 311	14.8	1.7	19	1	ADM34090	Mouse RIKEN 492151
C 312	14.8	1.7	19	1	ADH08028	Human glucose-6-ph
C 313	14.4	1.6	17	1	AAK23007	Integrin subunit b
C 314	14.4	1.6	17	1	AAV05438	Hammerhead ribozym
C 315	14.4	1.6	17	1	AAV03384	Hammerhead ribozym
C 316	14.4	1.6	17	1	AAV03381	Hammerhead ribozym
C 317	14.4	1.6	17	1	ABK02234	Human NOGO DNzyme
C 318	14.4	1.6	17	1	ABK02234	Human NOGO DNzyme
C 319	14.4	1.6	17	1	ABT37806	Tumour suppression
C 320	14.4	1.6	17	1	ABT37806	Tumour suppression
C 321	14.4	1.6	17	1	ACF62525	Cancer based on CY
C 322	14.4	1.6	17	1	ACF62524	Cancer based on CY
C 323	14.4	1.6	17	1	ADB21195	MRP1 based cancer
C 324	14.4	1.6	17	1	ADB21196	MRP1 based cancer
C 325	14.4	1.6	17	1	ADB88285	Human UGT1A1 varia
C 326	14.4	1.6	17	1	ADB88284	Human UGT1A1 varia
C 327	14.4	1.6	17	1	ADB97267	Human MDR1 variant
C 328	14.4	1.6	17	1	ADB97268	Human MDR1 variant
C 329	14.4	1.6	17	1	ADB92459	Human MDR1 variant
C 330	14.4	1.6	17	1	ADB92458	Human MDR1 variant
C 331	14.4	1.6	17	1	ADB44992	Tumour suppression
C 332	14.4	1.6	17	1	ADL48262	Human tumour suppressor
C 333	14.4	1.6	17	1	ABZ76052	Anticense inhibitor
C 334	14.4	1.6	18	1	ADK00139	Primer of the inve
C 335	14.4	1.6	18	1	AAZ32081	Xylulokinase PCR p
C 336	14.4	1.6	19	1	AAH83961	Cyclin A2 ribozyme
C 337	14.4	1.6	19	1	AAH59123	Cyclin A2 ribozyme
C 338	14.4	1.6	19	1	ADR77596	Human apolipoprote
C 339	14.4	1.6	19	1	ADR79231	Human apolipoprote
C 340	14.4	1.6	19	1	ADR74990	Common primer for
C 341	14	1.6	17	1	AAV81501	Human c-myb hammer
C 342	14	1.6	17	1	AAV81503	Human c-myb hammer
C 343	14	1.6	17	1	AAV81500	Human c-myb hammer
C 344	14	1.6	17	1	AAV81502	Human c-myb hammer
C 345	14	1.6	17	1	ABK01349	Human NOGO Inozyme
C 346	14	1.6	17	1	ABK00484	Human NOGO Hammerh
C 347	14	1.6	17	1	ABK01996	Human NOGO Zinzyme
C 348	14	1.6	17	1	ACA08316	Necrosis factor ka
C 349	14	1.6	17	1	ACA09130	NFKB sub-unit modu
C 350	14	1.6	20	1	ACC40921	Human superoxide d
C 351	14	1.6	20	1	ACC40922	Human superoxide d
C 352	13.8	1.6	17	1	AAV73200	Mouse fix-1 VEGF r
C 353	13.8	1.6	17	1	AAV96545	Potato citrate syn
C 354	13.8	1.6	17	1	AAV04937	Hammerhead ribozym
C 355	13.8	1.6	17	1	AAV04936	Hammerhead ribozym
C 356	13.8	1.6	17	1	AAV04935	Hammerhead ribozym
C 357	13.8	1.6	17	1	ABK01097	Human NOGO Inozyme
C 358	13.8	1.6	17	1	ABA80297	MLH1 mutation corr
C 359	13.8	1.6	17	1	ABA80296	MLH1 mutation corr
C 360	13.8	1.6	17	1	AAV91029	Human multi drug r
C 361	13.8	1.6	17	1	ABN08968	Human GDMPL-1 17-m
C 362	13.8	1.6	17	1	ACN03785	WNV Zinzyme subetr
C 363	13.8	1.6	17	1	ADB03682	Human MDZ7 scannin
C 364	13.8	1.6	17	1	ACD62281	HCV minus strand D
C 365	13.8	1.6	17	1	ADF62659	Human PCP1 DNA fr
C 366	13.8	1.6	17	1	ADL51188	Human PTGDR subetr
C 367	13.8	1.6	17	1	ADL51187	Human PTGDR subetr
C 368	13.8	1.6	17	1	ADL51536	Human PTGDR subetr
C 369	13.8	1.6	17	1	ADL55511	HCV DNzyme subetr
C 370	13.8	1.6	18	1	ACN72058	Human GDMPL-1 prob
C 371	13.8	1.6	18	1	AAV16415	Primer #2 for eWS
C 372	13.8	1.6	18	1	AAV05715	Maize retinoblasto
C 373	13.8	1.6	18	1	AAV17082	Maize retinoblasto
C 374	13.8	1.6	18	1	AAV85777	PCR primer used to
C 375	13.8	1.6	18	1	AAV85777	Human OB gene sequ
C 376	13.8	1.6	18	1	AAV85777	Cdc 2 kinase hamme
C 377	13.8	1.6	18	1	AAV85777	Human Ets-2 phosph
C 378	13.8	1.6	18	1	AAV12332	Human OB DNA PCR p
C 379	13.8	1.6	18	1	AAV251716	Burkholderia cepac
C 380	13.8	1.6	18	1	AAV251716	Human OB gene sequ
C 381	13.8	1.6	18	1	AAH61786	Cdc 2 kinase hamme
C 382	13.8	1.6	18	1	ABX89564	Human sequence tag
C 383	13.8	1.6	18	1	ABL61438	Human Ob gene STS
C 384	13.8	1.6	18	1	ABZ10441	Haematopoietic cel
C 385	13.8	1.6	18	1	ABZ10441	Human obese (ob) g
C 386	13.8	1.6	18	1	ADC69987	Primer oligo used
C 387	13.8	1.6	18	1	ADB84339	Human lymphoid cel
C 388	13.8	1.6	18	1	ADP78324	Chromosomal abnorm
C 389	13.8	1.6	18	1	ADH53129	Human APC (adenoma
C 390	13.8	1.6	18	1	ADR97900	Human APC DNA frag
C 391	13.8	1.6	18	1	ADS08584	Human DNA oligonuc
C 392	13.4	1.5	15	1	AAV50921	TGF-I oligonucleot
C 393	13.4	1.5	15	1	AAV46599	IgfBFB oligonucleo
C 394	13.4	1.5	15	1	ADO43607	Mutant DNA fragmen
C 395	13.4	1.5	15	1	ADO43602	DNA fragment from
C 396	13.4	1.5	16	1	AAV15510	N-acetyltransferas
C 397	13.4	1.5	16	1	ABT13505	Liver regeneration
C 398	13.4	1.5	16	1	ABZ68236	Probe/PCR primer f

C 107	20	2.3	20	1	ACCA0927	Human superoxide d	C 180	17.2	2.0	22	1	ACD23495	Human PRO PCR prim
C 108	20	2.3	20	1	ADQ80681	Human cytosolic su	C 181	17.2	2.0	22	1	ADB77533	Human secreted/tra
C 109	20	2.3	20	1	ADR42714	SOD gene analysis	C 182	17.2	2.0	22	1	ADB74669	Human secreted/tra
C 110	20	2.3	20	1	ADR42715	SOD gene analysis	C 183	17.2	2.0	22	1	ADC28315	Human secreted/tra
C 111	20	2.3	21	1	AAQ67477	PCR primer for hum	C 184	17.2	2.0	22	1	ADC39515	Human secreted/tra
C 112	20	2.3	21	1	AAV73827	Human SOD1 exon 1	C 185	17.2	2.0	22	1	ADC40029	Human secreted/tra
C 113	20	2.3	21	1	ADQ55690	Human cytosolic su	C 186	17.2	2.0	22	1	ADC18857	Human secreted/tra
C 114	20	2.3	25	1	ADQ43049	Short interfering	C 187	17.2	2.0	22	1	ADC34153	Human secreted/tra
C 115	19.8	2.3	23	1	ABQ75418	CuZn superoxide di	C 188	17.2	2.0	22	1	ADC29208	Human secreted/tra
C 116	19.4	2.2	21	1	ADQ52404	Target DNA sequenc	C 189	17.2	2.0	22	1	ADC28739	Human secreted/tra
C 117	19.4	2.2	21	1	ADQ52403	Target DNA sequenc	C 190	17.2	2.0	22	1	ADC40624	Human secreted/tra
C 118	19.4	2.2	22	1	AAH81808	Probe used to iden	C 191	17.2	2.0	22	1	ADC19281	Human secreted/tra
C 119	19.4	2.2	25	1	ADQ43051	Short interfering	C 192	17.2	2.0	22	1	ADC33729	Human secreted/tra
C 120	19.2	2.2	23	1	ADQ52415	siRNA p9 sequence	C 193	17.2	2.0	22	1	ADC12799	Human secreted/tra
C 121	19.2	2.2	23	1	ADQ52417	siRNA p11 sequence	C 194	17.2	2.0	22	1	ADC12251	Human secreted/tra
C 122	19	2.2	19	1	AAH60181	Sequence of probe	C 195	17.2	2.0	22	1	ADD04806	Human secreted/tra
C 123	19	2.2	19	1	ABQ73056	Cu/Zn SOD gene rel	C 196	17.2	2.0	22	1	ADD03812	Human secreted/tra
C 124	19	2.2	19	1	ADQ80680	Human cytosolic su	C 197	17.2	2.0	22	1	ADD03388	Human secreted/tra
C 125	19	2.2	23	1	ADQ52425	siRNA p11 sequence	C 198	17.2	2.0	22	1	ADQ34540	Human secreted/tra
C 126	19	2.2	23	1	ADQ52424	siRNA p10 sequence	C 199	17.2	2.0	22	1	ADH59123	Human secreted/tra
C 127	19	2.2	23	1	ADQ52423	siRNA p9 sequence	C 200	17.2	2.0	22	1	ADH59123	Human secreted/tra
C 128	19	2.2	25	1	ADQ43052	Short interfering	C 201	17.2	2.0	22	1	ACA58900	Human secreted/tra
C 129	19	2.2	25	1	ADQ43053	Short interfering	C 202	17.2	2.0	22	1	ACA58297	PCR primer #2 used
C 130	19	2.2	25	1	ADQ43050	Short interfering	C 203	17.2	2.0	22	1	ADJ26170	Human secreted/tra
C 131	19	2.2	25	1	ADQ43054	Short interfering	C 204	17.2	2.0	22	1	ADJ26170	Human secreted/tra
C 132	18.4	2.1	20	1	AAV01384	Superoxide dismuta	C 205	17.2	2.0	22	1	ADH79085	Human secreted/tra
C 133	18.2	2.1	24	1	ADD26381	RT-PCR primer #2 f	C 206	17.2	2.0	22	1	ADH79509	Human secreted/tra
C 134	18	2.1	18	1	ADH766494	PCR primer for CuZ	C 207	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 135	18	2.1	23	1	ADH52416	siRNA p10 sequence	C 208	17.2	2.0	22	1	ADH73720	Human secreted/tra
C 136	18	2.1	23	1	ADH52411	Mutant siRNA p10 s	C 209	17.2	2.0	22	1	ADH99274	Human secreted/tra
C 137	17.6	2.0	23	1	ADH52410	Mutant siRNA p11 s	C 210	17.2	2.0	22	1	ADH98820	Human secreted/tra
C 138	17.6	2.0	23	1	ADH52412	Mutant siRNA p9 se	C 211	17.2	2.0	22	1	ADG40290	Human secreted/tra
C 139	17.4	2.0	19	1	ADH52401	Target DNA sequenc	C 212	17.2	2.0	22	1	ADG40290	Human secreted/tra
C 140	17.4	2.0	19	1	ADH52402	Target DNA sequenc	C 213	17.2	2.0	22	1	ADF73684	Human secreted/tra
C 141	17.4	2.0	20	1	ABZ91893	Human oligonucleot	C 214	17.2	2.0	22	1	ADG92103	Human secreted/tra
C 142	17.4	2.0	20	1	ABD28123	AA156940-derived o	C 215	17.2	2.0	22	1	ADG92530	Human secreted/tra
C 143	17.4	2.0	21	1	ABZ98129	Human multidrug re	C 216	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 144	17.4	2.0	23	1	ADH52421	Mutant siRNA p10 s	C 217	17.2	2.0	22	1	ADH07174	Human secreted/tra
C 145	17.4	2.0	23	1	ADH52420	Mutant siRNA p11 s	C 218	17.2	2.0	22	1	ADH59719	Human secreted/tra
C 146	17.4	2.0	23	1	ADH52422	Mutant siRNA p9 se	C 219	17.2	2.0	22	1	ADH06747	Human secreted/tra
C 147	17.2	2.0	22	1	AAH28452	EGF-like/FGF-8 hom	C 220	17.2	2.0	22	1	ADI18489	Human secreted/tra
C 148	17.2	2.0	22	1	AAH37608	Human PRO217 prime	C 221	17.2	2.0	22	1	ADI65209	Human secreted/tra
C 149	17.2	2.0	22	1	AAH52278	Primer 28730.r (OL	C 222	17.2	2.0	22	1	ADI37472	Human secreted/tra
C 150	17.2	2.0	22	1	AAH52278	Primer for amplify	C 223	17.2	2.0	22	1	ADH97276	Human secreted/tra
C 151	17.2	2.0	22	1	AAH30042	Reverse PCR primer	C 224	17.2	2.0	22	1	ADH65636	Human secreted/tra
C 152	17.2	2.0	22	1	AAH52217	Reverse primer 287	C 225	17.2	2.0	22	1	ADH60379	Human secreted/tra
C 153	17.2	2.0	22	1	AAH54087	Primer for amplify	C 226	17.2	2.0	22	1	ADJ99436	Human secreted/tra
C 154	17.2	2.0	22	1	AAH54087	Human PRO protein-	C 227	17.2	2.0	22	1	ADL08629	Human secreted/tra
C 155	17.2	2.0	22	1	AAH72436	Human PRO oligonuc	C 228	17.2	2.0	22	1	ADM24974	Human secreted/tra
C 156	17.2	2.0	22	1	AAH00172	PCR primer 4 for H	C 229	17.2	2.0	22	1	ADM24974	Human secreted/tra
C 157	17.2	2.0	22	1	AAH97412	Human PRO211 PCR p	C 230	17.2	2.0	22	1	ADO06042	Human secreted/tra
C 158	17.2	2.0	22	1	AAH60362	PRO211 reverse PCR	C 231	17.2	2.0	22	1	ADR10894	Human secreted/tra
C 159	17.2	2.0	22	1	ACA60004	Human secreted/tra	C 232	17.2	2.0	22	1	ADR17803	Human secreted/tra
C 160	17.2	2.0	22	1	ACD07404	Secreted and trans	C 233	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 161	17.2	2.0	22	1	ABX71452	Human secreted/tra	C 234	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 162	17.2	2.0	22	1	ACH06784	Human secreted/tra	C 235	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 163	17.2	2.0	22	1	ABX96021	Human secreted/tra	C 236	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 164	17.2	2.0	22	1	ACA05342	Human secreted pro	C 237	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 165	17.2	2.0	22	1	ACD20009	Human secreted / t	C 238	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 166	17.2	2.0	22	1	ACA54812	Secreted and trans	C 239	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 167	17.2	2.0	22	1	ACD19647	Human secreted / t	C 240	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 168	17.2	2.0	22	1	ADH29212	Human secreted/tra	C 241	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 169	17.2	2.0	22	1	ADA18068	Human secreted/tra	C 242	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 170	17.2	2.0	22	1	ACD66794	Human secreted/tra	C 243	17.2	2.0	22	1	AAQ67479	Human secreted/tra
C 171	17.2	2.0	22	1	ACD82955	Human PRO PCR prim	C 244	17.2	2.0	22	1	AAV73829	Human secreted/tra
C 172	17.2	2.0	22	1	ADA16043	Human secreted/tra	C 245	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 173	17.2	2.0	22	1	ADA24188	Human secreted/tra	C 246	17.2	2.0	22	1	ADT03479	Human secreted/tra
C 174	17.2	2.0	22	1	ACD23133	Human PRO PCR prim	C 247	16.8	1.9	20	1	AAH93934	Mouse SOD-1 exon 4
C 175	17.2	2.0	22	1	ADA16467	Human secreted/tra	C 248	16.8	1.9	20	1	AAH93934	Primer for exon 23
C 176	17.2	2.0	22	1	ADA12896	Human secreted/tra	C 249	16.8	1.9	21	1	AAQ67482	PCR primer for hum
C 177	17.2	2.0	22	1	ADA41764	Human secreted/tra	C 250	16.8	1.9	21	1	AAV73832	Human SOD1 exon 4
C 178	17.2	2.0	22	1	ADA17111	Human secreted/tra	C 251	16.4	1.9	20	1	ADT03479	Human cytosolic su
C 179	17.2	2.0	22	1	ADA42614	Human secreted/tra	C 252	16.4	1.9	20	1	ADT03479	Human cytosolic su

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 CompuGen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: October 6, 2005, 10:44:11 ; Search time 6 Seconds
 (without alignments)
 3.425 Million cell updates/sec
 Title: US-10-633-843-3-COPY
 Perfect score: 874
 Sequence: 1 ctgcagctcgtgggtttcc.....tattaaagaatccaattc 874
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 0.5
 Searched: 608 seqs, 11755 residues
 Total number of hits satisfying chosen parameters: 1216
 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 610 summaries
 Database : ngsdb.*

N. Geneseg

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.7	50	1	ABZ00314 Human leukocyte ge
2	50	5.7	50	1	ABZ01960 Human leukocyte ge
3	48	5.5	48	1	AD52413 Wild-type human SO
4	48	5.5	48	1	ADO43047 Superoxide dismuta
5	46.4	5.3	48	1	AD52414 Human SOD1 mutant
6	46.4	5.3	48	1	ADO43048 Superoxide dismuta
7	40	4.6	40	1	AAQ27817 Primer A039. Synt
8	35	4.0	35	1	AD52418 Wild-type human SO
9	35	4.0	35	1	ADO43055 Superoxide dismuta
10	28	3.2	28	1	ABK66923 Human gene specifi
11	28	3.2	28	1	ABK66924 Human gene specifi
12	27	3.1	27	1	ABA94683 Antisense S-oligo
13	25	2.9	33	1	ADQ75020 Human superoxide d
14	24	2.7	24	1	AAQ67485 PCR primer for hum
15	24	2.7	24	1	AAV73935 Human SOD1 exon 5
16	24	2.7	24	1	ADO55698 Human cytosolic su
17	23	2.6	23	1	ABA94686 Superoxide dismuta
18	23	2.6	23	1	ABA94685 Superoxide dismuta
19	23	2.6	23	1	ABX12365 Oxidative stress d
20	23	2.6	23	1	ABX12364 Oxidative stress d
21	22.6	2.6	30	1	AA888339 Mouse (balb/c) for
22	22.6	2.6	30	1	AA888339 Mouse Cu/Zn-SOD (s
23	22.4	2.6	25	1	ABD13501 Rat superoxide dis
24	22.2	2.5	27	1	AD29666 Human Zn-SOD ampli
25	22.2	2.5	27	1	ADO59161 Human Cu/Zn-supero
26	22.2	2.5	27	1	ADQ06573 Fusion protein rel
27	22.2	2.5	27	1	ADQ74975 Tat-pyridoxal kina
28	22	2.5	22	1	ADG73925 Human superoxide d
29	22	2.5	22	1	ADG73926 Human superoxide d
30	22	2.5	27	1	ADG59160 Human Cu/Zn-supero
31	22	2.5	27	1	ADQ06572 Fusion protein rel
32	22	2.5	27	1	ADQ74974 Tat-pyridoxal kina
33	22	2.5	29	1	AAV32582 Human SOD-1 cDNA p

C	34	21	2.4	21	1	ABQ73054 Cu/Zn SOD gene rel
C	35	21	2.4	21	1	ABZ79578 Human superoxide d
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C	38	21	2.4	21	1	ADT66493 PCR primer for CuZ
C	39	20.4	2.3	20	1	ABQ73057 Cu/Zn SOD gene rel
C	40	20	2.3	20	1	AAV011383 Superoxide dismuta
C	41	20	2.3	20	1	ACC40898 Human superoxide d
C	42	20	2.3	20	1	ACC40912 Human superoxide d
C	43	20	2.3	20	1	ACC40914 Human superoxide d
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c 159	12.8	1.5	17	1	US-09-720-435A-191	Sequence 191, Appl
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c 166	12.4	1.4	15	1	US-08-363-240A-145	Sequence 145, Appl
c 167	12.4	1.4	15	1	US-08-774-310-197	Sequence 197, Appl
c 168	12.4	1.4	15	1	US-09-531-000-9	Sequence 9, Appl
c 169	12.4	1.4	16	1	US-09-371-772B-5681	Sequence 5681, Ap
c 170	12	1.4	15	1	US-08-319-492B-148	Sequence 148, Appl
c 171	12	1.4	15	1	US-08-363-240A-143	Sequence 143, Appl
c 172	12	1.4	15	1	US-08-635-309-24	Sequence 24, Appl
c 173	12	1.4	15	1	US-08-585-684B-2103	Sequence 2103, Ap
c 174	12	1.4	15	1	US-09-038-073-2103	Sequence 31, Appl
c 175	12	1.4	16	1	US-08-173-489C-31	Sequence 31, Appl
c 176	12	1.4	16	1	US-09-371-772B-6963	Sequence 6963, Ap
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c 178	12	1.4	17	1	US-08-373-124A-964	Sequence 964, Appl
c 179	12	1.4	17	1	US-08-373-124A-966	Sequence 966, Appl

ALIGNMENTS

RESULT 1

US-08-859-998-1011
 ; Sequence 1011, Application US/08859998
 ; Patent No. 5994076
 ; GENERAL INFORMATION:
 ; APPLICANT: Chenchik, Alex
 ; APPLICANT: Jochadze, George
 ; APPLICANT: Bibilashvili, Robert
 ; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
 ; TITLE OF INVENTION: EXPRESSION
 ; NUMBER OF SEQUENCES: 1375
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Fish & Richardson, P.C.
 ; STREET: 2200 Sand Hill Road, Suite 100
 ; CITY: Menlo Park
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94025
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/859,998
 ; FILING DATE: 21-MAY-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Field, Bret E.
 ; REGISTRATION NUMBER: 37,620
 ; REFERENCE/DOCKET NUMBER: 09096/002001
 ; TELEPHONE: 415-322-5070
 ; TELEFAX: 415-854-0875
 ; INFORMATION FOR SEQ ID NO: 1011:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 28 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide primer
 ; US-08-859-998-1011

Query Match 3.2%; Score 28; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 106 AGTCAGGCGCATCATCAATTTGAGCAG 133

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:41:23 ; Search time 2 Seconds
(without alignments)
2.994 Million cell updates/sec

Title: US-10-633-843-3-COPY
Perfect score: 874
Sequence: 1 ctcgagcgtctgggtttcc.....tattaaagaatccaaattc 874

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 188 seqs, 3426 residues

Total number of hits satisfying chosen parameters: 376

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 194 summaries

Database : issdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	3.2	28	1	US-08-859-998-1011
2	28	3.2	28	1	US-08-859-998-1012
3	28	3.2	28	1	US-09-225-928-1011
4	28	3.2	28	1	US-09-225-928-1012
5	28	3.2	28	1	US-09-225-201B-1011
6	28	3.2	28	1	US-09-225-201B-1012
7	24	2.7	24	1	US-08-023-980B-18
8	24	2.7	24	1	US-08-486-953A-13
9	24	2.7	24	1	US-08-204-052-13
10	22	2.5	29	1	US-08-868-381A-2
11	21.8	2.5	25	1	5290690-19
12	21.8	2.5	25	1	5290690-19
13	20	2.3	21	1	US-08-023-980B-5
14	20	2.3	21	1	US-08-486-953A-5
15	20	2.3	21	1	US-08-204-052-5
16	17.2	2.0	22	1	US-09-907-794A-7
17	17.2	2.0	22	1	US-09-905-125A-7
18	17.2	2.0	22	1	US-09-302-775A-7
19	17.2	2.0	22	1	US-09-906-700-7
20	17.2	2.0	22	1	US-09-903-603A-7
21	17.2	2.0	22	1	US-09-304-920A-7
22	17.2	2.0	22	1	US-09-909-064-7
23	17.2	2.0	22	1	US-09-905-381A-7
24	17.2	2.0	22	1	US-09-906-618-7
25	17.2	2.0	22	1	5290690-20
26	17.2	2.0	22	1	5290690-20
27	17	1.9	21	1	US-08-023-980B-7
28	17	1.9	21	1	US-08-486-953A-7
29	17	1.9	21	1	US-08-204-052-7
30	16.8	1.9	20	1	US-09-068-506-48
31	16.8	1.9	21	1	US-08-023-980B-10
32	16.8	1.9	21	1	US-08-486-953A-10
33	16.8	1.9	21	1	US-08-204-052-10

34	16	1.8	19	1	US-09-545-686-27	Sequence 27, Appl
35	15.8	1.8	20	1	US-08-202-042-2	Sequence 2, Appl
36	15.8	1.8	20	1	US-09-060-299-236	Sequence 236, Appl
37	15.8	1.8	20	1	US-09-402-922A-236	Sequence 236, Appl
38	15.8	1.8	20	1	US-09-909-595-79	Sequence 79, Appl
39	15.2	1.7	20	1	US-09-040-285A-4	Sequence 4, Appl
40	15.2	1.7	20	1	US-09-288-461-39	Sequence 39, Appl
41	15.2	1.7	20	1	US-09-758-881-39	Sequence 39, Appl
42	15	1.7	20	1	US-08-846-020A-17	Sequence 17, Appl
43	15	1.7	20	1	US-09-617-871-17	Sequence 17, Appl
44	14.8	1.7	19	1	US-09-108-006C-31	Sequence 31, Appl
45	14.8	1.7	19	1	US-09-696-791-574	Sequence 574, Appl
46	14.4	1.6	17	1	US-08-412-614-102	Sequence 102, Appl
47	14.4	1.6	17	1	US-08-412-614-104	Sequence 104, Appl
48	14.4	1.6	17	1	US-08-635-761-102	Sequence 102, Appl
49	14.4	1.6	17	1	US-09-312-520-102	Sequence 102, Appl
50	14.4	1.6	17	1	US-09-312-520-104	Sequence 104, Appl
51	14.4	1.6	17	1	US-09-312-520-104	Sequence 104, Appl
52	14.4	1.6	17	1	US-09-863-086-102	Sequence 102, Appl
53	14.4	1.6	17	1	US-09-863-086-104	Sequence 104, Appl
54	14.4	1.6	19	1	US-09-696-791-1547	Sequence 1547, Ap
55	14	1.6	17	1	US-08-373-124A-962	Sequence 962, Appl
56	14	1.6	17	1	US-08-373-124A-964	Sequence 964, Appl
57	14	1.6	17	1	US-08-373-124A-966	Sequence 966, Appl
58	14	1.6	17	1	US-08-435-628-962	Sequence 962, Appl
59	14	1.6	17	1	US-08-435-628-964	Sequence 964, Appl
60	14	1.6	17	1	US-08-435-628-966	Sequence 966, Appl
61	13.8	1.6	17	1	US-08-584-040-5950	Sequence 5950, Ap
62	13.8	1.6	17	1	US-09-371-772B-2787	Sequence 2787, Ap
63	13.8	1.6	17	1	US-09-371-772B-5100	Sequence 5100, Ap
64	13.8	1.6	17	1	US-09-371-772B-6796	Sequence 6796, Ap
65	13.8	1.6	17	1	US-09-866-108A-8960	Sequence 8960, Ap
66	13.8	1.6	17	1	US-09-685-664B-2787	Sequence 2787, Ap
67	13.8	1.6	18	1	US-08-379-081B-88	Sequence 88, Appl
68	13.8	1.6	18	1	US-08-379-081B-89	Sequence 89, Appl
69	13.8	1.6	18	1	US-08-379-081B-90	Sequence 90, Appl
70	13.8	1.6	18	1	US-08-379-081B-91	Sequence 91, Appl
71	13.8	1.6	18	1	US-08-379-081B-92	Sequence 92, Appl
72	13.8	1.6	18	1	US-08-379-081B-93	Sequence 93, Appl
73	13.8	1.6	18	1	US-08-379-081B-94	Sequence 94, Appl
74	13.8	1.6	18	1	US-08-379-081B-95	Sequence 95, Appl
75	13.8	1.6	18	1	US-08-379-081B-96	Sequence 96, Appl
76	13.8	1.6	18	1	US-08-379-081B-97	Sequence 97, Appl
77	13.8	1.6	18	1	US-08-379-081B-98	Sequence 98, Appl
78	13.8	1.6	18	1	US-08-379-081B-99	Sequence 99, Appl
79	13.8	1.6	18	1	US-08-379-081B-100	Sequence 100, Appl
80	13.8	1.6	18	1	US-08-379-078-88	Sequence 88, Appl
81	13.8	1.6	18	1	US-08-379-078-89	Sequence 89, Appl
82	13.8	1.6	18	1	US-08-379-078-90	Sequence 90, Appl
83	13.8	1.6	18	1	US-08-379-078-91	Sequence 91, Appl
84	13.8	1.6	18	1	US-08-379-078-92	Sequence 92, Appl
85	13.8	1.6	18	1	US-08-379-078-93	Sequence 93, Appl
86	13.8	1.6	18	1	US-08-379-078-94	Sequence 94, Appl
87	13.8	1.6	18	1	US-08-379-078-95	Sequence 95, Appl
88	13.8	1.6	18	1	US-08-379-078-96	Sequence 96, Appl
89	13.8	1.6	18	1	US-08-379-078-97	Sequence 97, Appl
90	13.8	1.6	18	1	US-08-379-078-98	Sequence 98, Appl
91	13.8	1.6	18	1	US-08-379-078-99	Sequence 99, Appl
92	13.8	1.6	18	1	US-08-379-078-100	Sequence 100, Appl
93	13.8	1.6	18	1	US-08-485-942A-62	Sequence 62, Appl
94	13.8	1.6	18	1	US-09-344-579-8	Sequence 8, Appl
95	13.8	1.6	18	1	US-08-488-214A-62	Sequence 62, Appl
96	13.8	1.6	18	1	US-08-488-208A-62	Sequence 62, Appl
97	13.8	1.6	18	1	US-08-488-211A-62	Sequence 62, Appl
98	13.8	1.6	18	1	US-08-488-223A-62	Sequence 62, Appl
99	13.8	1.6	18	1	US-08-438-431A-62	Sequence 62, Appl
100	13.8	1.6	18	1	US-08-488-225A-62	Sequence 62, Appl
101	13.8	1.6	18	1	US-09-696-791-4190	Sequence 4190, Ap
102	13.8	1.6	18	1	US-09-599-003-7	Sequence 7, Appl
103	13.4	1.5	16	1	US-09-371-772B-5942	Sequence 5942, Ap
104	13.4	1.5	17	1	US-08-584-040-4278	Sequence 4278, Ap
105	13.4	1.5	17	1	US-08-584-040-4279	Sequence 4279, Ap
106	13.4	1.5	17	1	US-08-584-040-7632	Sequence 7632, Ap

Issued - Patents - N/A

326	12.8	1.5	17	1	AX735466	ACCESSION:AX735466
327	12.8	1.5	17	1	AX736213	ACCESSION:AX736213
328	12.8	1.5	17	1	AX736475	ACCESSION:AX736475
329	12.8	1.5	17	1	AX737257	ACCESSION:AX737257
330	12.8	1.5	17	1	AX737808	ACCESSION:AX737808
331	12.8	1.5	17	1	AX738774	ACCESSION:AX738774
332	12.8	1.5	17	1	AX739446	ACCESSION:AX739446
333	12.8	1.5	17	1	AX739528	ACCESSION:AX739528
334	12.8	1.5	17	1	AX757321	ACCESSION:AX757321
335	12.8	1.5	17	1	AX757495	ACCESSION:AX757495
336	12.8	1.5	17	1	AX759535	ACCESSION:AX759535
337	12.8	1.5	17	1	AX759882	ACCESSION:AX759882
338	12.8	1.5	17	1	AX761187	ACCESSION:AX761187
339	12.8	1.5	17	1	AX782229	ACCESSION:AX782229
340	12.8	1.5	17	1	AX782230	ACCESSION:AX782230
341	12.8	1.5	17	1	AX782231	ACCESSION:AX782231
342	12.8	1.5	17	1	AX782233	ACCESSION:AX782233
343	12.8	1.5	17	1	BD066052	ACCESSION:BD066052
344	12.8	1.5	17	1	BD067878	ACCESSION:BD067878
345	12.8	1.5	17	1	BD104610	ACCESSION:BD104610
346	12.4	1.4	14	1	CQ821410	ACCESSION:CQ821410
347	12.4	1.4	14	1	AX081113	ACCESSION:AX081113
348	12.4	1.4	15	1	I35229	ACCESSION:I35229
349	12.4	1.4	15	1	AX085048	ACCESSION:AX085048
350	12.4	1.4	16	1	A35583	ACCESSION:A35583
351	12.4	1.4	16	1	AR235510	ACCESSION:AR235510
352	12.4	1.4	16	1	AR328279	ACCESSION:AR328279
353	12.4	1.4	16	1	AX099234	ACCESSION:AX099234
354	12.4	1.4	16	1	AX050960	ACCESSION:AX050960
355	12	1.4	14	1	CQ828340	ACCESSION:CQ828340
356	12	1.4	15	1	AR133678	ACCESSION:AR133678
357	12	1.4	15	1	I39110	ACCESSION:I39110
358	12	1.4	15	1	I80907	ACCESSION:I80907
359	12	1.4	15	1	AX377090	ACCESSION:AX377090
360	12	1.4	15	1	AX635353	ACCESSION:AX635353
361	12	1.4	16	1	AR029842	ACCESSION:AR029842
362	12	1.4	16	1	AR329561	ACCESSION:AR329561
363	12	1.4	16	1	BD104793	ACCESSION:BD104793

RESULT 1

ACCESSION AR090891
VERSION AR090891.1 GI:10017646

ORGANISM	Unknown.	Incl aggr

AUTHORS	Chencklik
TITLE	Methods

source

Query Match

Q. Now, you're going to tell me that the defendant was not in the car at the time of the shooting, is that correct?

Db 1 AGTGCA(

AR090892/c

C 107	14.4	1.6	17	1	AX216792	ACCSSION:AX216792	180	13.8	1.6	18	1	AX796133	ACCESSION:AX796133
C 108	14.4	1.6	17	1	AX216884	ACCESSION:AX216884	C 181	13.8	1.6	18	1	BD014805	ACCESSION:BD014805
C 109	14.4	1.6	17	1	AX701183	ACCESSION:AX701183	182	13.4	1.5	15	1	CQ821404	ACCESSION:CQ821404
C 110	14.4	1.6	17	1	AX706656	ACCESSION:AX706656	183	13.4	1.5	15	1	CQ821409	ACCESSION:CQ821409
C 111	14.4	1.6	17	1	AX706657	ACCESSION:AX706657	C 184	13.4	1.5	16	1	BD178695	ACCESSION:BD178695
C 112	14.4	1.6	17	1	AX707586	ACCESSION:AX707586	C 185	13.4	1.5	16	1	AX328540	ACCESSION:AX328540
C 113	14.4	1.6	17	1	AX707587	ACCESSION:AX707587	C 186	13.4	1.5	16	1	AX600643	ACCESSION:AX600643
C 114	14.4	1.6	17	1	AX731809	ACCESSION:AX731809	C 187	13.4	1.5	17	1	BD255583	ACCESSION:BD255583
C 115	14.4	1.6	17	1	AX733720	ACCESSION:AX733720	188	13.4	1.5	17	1	AR188790	ACCESSION:AR188790
C 116	14.4	1.6	17	1	AX735175	ACCESSION:AX735175	189	13.4	1.5	17	1	AR188791	ACCESSION:AR188791
C 117	14.4	1.6	17	1	AX761994	ACCESSION:AX761994	C 190	13.4	1.5	17	1	AR192144	ACCESSION:AR192144
C 118	14.4	1.6	17	1	CQ784352	ACCESSION:CQ784352	C 191	13.4	1.5	17	1	AR192145	ACCESSION:AR192145
C 119	14.4	1.6	19	1	E31531	ACCESSION:E31531	192	13.4	1.5	17	1	AR324643	ACCESSION:AR324643
C 120	14.4	1.6	19	1	AX130329	ACCESSION:AX130329	193	13.4	1.5	17	1	AR324644	ACCESSION:AR324644
C 121	14	1.6	17	1	AR046169	ACCESSION:AR046169	C 194	13.4	1.5	17	1	AR326022	ACCESSION:AR326022
C 122	14	1.6	17	1	AR046171	ACCESSION:AR046171	C 195	13.4	1.5	17	1	AR326023	ACCESSION:AR326023
C 123	14	1.6	17	1	AR046173	ACCESSION:AR046173	C 196	13.4	1.5	17	1	AX214956	ACCESSION:AX214956
C 124	14	1.6	17	1	I53221	ACCESSION:I53221	C 197	13.4	1.5	17	1	AX265895	ACCESSION:AX265895
C 125	14	1.6	17	1	I53223	ACCESSION:I53223	C 198	13.4	1.5	17	1	AX265896	ACCESSION:AX265896
C 126	14	1.6	17	1	I53225	ACCESSION:I53225	C 199	13.4	1.5	17	1	AX728909	ACCESSION:AX728909
C 127	14	1.6	17	1	AX215042	ACCESSION:AX215042	200	13.4	1.5	17	1	AX729782	ACCESSION:AX729782
C 128	14	1.6	17	1	AX215907	ACCESSION:AX215907	201	13.4	1.5	17	1	AX732168	ACCESSION:AX732168
C 129	14	1.6	17	1	AX216554	ACCESSION:AX216554	C 202	13.4	1.5	17	1	AX732908	ACCESSION:AX732908
C 130	13.8	1.6	17	1	BD257133	ACCESSION:BD257133	C 203	13.4	1.5	17	1	AX737665	ACCESSION:AX737665
C 131	13.8	1.6	17	1	BD257134	ACCESSION:BD257134	204	13.4	1.5	17	1	AX761865	ACCESSION:AX761865
C 132	13.8	1.6	17	1	BD257135	ACCESSION:BD257135	205	13	1.5	13	1	BD263834	ACCESSION:BD263834
C 133	13.8	1.6	17	1	CQ624220	ACCESSION:CQ624220	206	13	1.5	13	1	BD263836	ACCESSION:BD263836
C 134	13.8	1.6	17	1	I06874	ACCESSION:I06874	207	13	1.5	13	1	BD263840	ACCESSION:BD263840
C 135	13.8	1.6	17	1	AR190462	ACCESSION:AR190462	C 208	13	1.5	13	1	BD263848	ACCESSION:BD263848
C 136	13.8	1.6	17	1	AR325385	ACCESSION:AR325385	209	13	1.5	13	1	AX048320	ACCESSION:AX048320
C 137	13.8	1.6	17	1	AR327698	ACCESSION:AR327698	210	13	1.5	13	1	AX048322	ACCESSION:AX048322
C 138	13.8	1.6	17	1	AR329394	ACCESSION:AR329394	211	13	1.5	13	1	AX048324	ACCESSION:AX048324
C 139	13.8	1.6	17	1	AR465283	ACCESSION:AR465283	212	13	1.5	13	1	AX048326	ACCESSION:AX048326
C 140	13.8	1.6	17	1	AX081872	ACCESSION:AX081872	C 213	13	1.5	16	1	CQ786469	ACCESSION:CQ786469
C 141	13.8	1.6	17	1	AX215655	ACCESSION:AX215655	214	13	1.5	16	1	AR329602	ACCESSION:AR329602
C 142	13.8	1.6	17	1	AX265751	ACCESSION:AX265751	215	13	1.5	17	1	AR186415	ACCESSION:AR186415
C 143	13.8	1.6	17	1	AX265752	ACCESSION:AX265752	216	13	1.5	17	1	AR323046	ACCESSION:AR323046
C 144	13.8	1.6	17	1	AX691936	ACCESSION:AX691936	217	13	1.5	17	1	AR327316	ACCESSION:AR327316
C 145	13.8	1.6	17	1	AX782232	ACCESSION:AX782232	218	13	1.5	17	1	AR328890	ACCESSION:AR328890
C 146	13.8	1.6	18	1	AR175662	ACCESSION:AR175662	C 219	13	1.5	17	1	AR328891	ACCESSION:AR328891
C 147	13.8	1.6	18	1	I30650	ACCESSION:I30650	C 220	13	1.5	17	1	AX215041	ACCESSION:AX215041
C 148	13.8	1.6	18	1	I30651	ACCESSION:I30651	C 221	13	1.5	17	1	AX215043	ACCESSION:AX215043
C 149	13.8	1.6	18	1	I30652	ACCESSION:I30652	C 222	13	1.5	17	1	AX726716	ACCESSION:AX726716
C 150	13.8	1.6	18	1	I30653	ACCESSION:I30653	223	12.8	1.5	16	1	AL0669	ACCESSION:AL0669
C 151	13.8	1.6	18	1	I30654	ACCESSION:I30654	224	12.8	1.5	16	1	CQ821403	ACCESSION:CQ821403
C 152	13.8	1.6	18	1	I30655	ACCESSION:I30655	C 225	12.8	1.5	16	1	AR328567	ACCESSION:AR328567
C 153	13.8	1.6	18	1	I30656	ACCESSION:I30656	226	12.8	1.5	16	1	AR328701	ACCESSION:AR328701
C 154	13.8	1.6	18	1	I30657	ACCESSION:I30657	227	12.8	1.5	16	1	AX040892	ACCESSION:AX040892
C 155	13.8	1.6	18	1	I30658	ACCESSION:I30658	C 228	12.8	1.5	17	1	A88539	ACCESSION:A88539
C 156	13.8	1.6	18	1	I30659	ACCESSION:I30659	C 229	12.8	1.5	17	1	A90506	ACCESSION:A90506
C 157	13.8	1.6	18	1	I30660	ACCESSION:I30660	230	12.8	1.5	17	1	AR110572	ACCESSION:AR110572
C 158	13.8	1.6	18	1	I30661	ACCESSION:I30661	231	12.8	1.5	17	1	AR151792	ACCESSION:AR151792
C 159	13.8	1.6	18	1	I30662	ACCESSION:I30662	C 232	12.8	1.5	17	1	BD141639	ACCESSION:BD141639
C 160	13.8	1.6	18	1	I46109	ACCESSION:I46109	C 233	12.8	1.5	17	1	BD142773	ACCESSION:BD142773
C 161	13.8	1.6	18	1	I46110	ACCESSION:I46110	C 234	12.8	1.5	17	1	BD200757	ACCESSION:BD200757
C 162	13.8	1.6	18	1	I46111	ACCESSION:I46111	C 235	12.8	1.5	17	1	BD201590	ACCESSION:BD201590
C 163	13.8	1.6	18	1	I46112	ACCESSION:I46112	C 236	12.8	1.5	17	1	BD201591	ACCESSION:BD201591
C 164	13.8	1.6	18	1	I46113	ACCESSION:I46113	237	12.8	1.5	17	1	BD232934	ACCESSION:BD232934
C 165	13.8	1.6	18	1	I46114	ACCESSION:I46114	C 238	12.8	1.5	17	1	BD233095	ACCESSION:BD233095
C 166	13.8	1.6	18	1	I46115	ACCESSION:I46115	C 239	12.8	1.5	17	1	BD241523	ACCESSION:BD241523
C 167	13.8	1.6	18	1	I46116	ACCESSION:I46116	C 240	12.8	1.5	17	1	BD256491	ACCESSION:BD256491
C 168	13.8	1.6	18	1	I46117	ACCESSION:I46117	C 241	12.8	1.5	17	1	BD256939	ACCESSION:BD256939
C 169	13.8	1.6	18	1	I46118	ACCESSION:I46118	242	12.8	1.5	17	1	BD257132	ACCESSION:BD257132
C 170	13.8	1.6	18	1	I46119	ACCESSION:I46119	243	12.8	1.5	17	1	BD257552	ACCESSION:BD257552
C 171	13.8	1.6	18	1	I46120	ACCESSION:I46120	C 244	12.8	1.5	17	1	BD258550	ACCESSION:BD258550
C 172	13.8	1.6	18	1	I46121	ACCESSION:I46121	C 245	12.8	1.5	17	1	BD258551	ACCESSION:BD258551
C 173	13.8	1.6	18	1	AR195238	ACCESSION:AR195238	246	12.8	1.5	17	1	CQ616850	ACCESSION:CQ616850
C 174	13.8	1.6	18	1	AR222320	ACCESSION:AR222320	247	12.8	1.5	17	1	CQ616851	ACCESSION:CQ616851
C 175	13.8	1.6	18	1	AR241439	ACCESSION:AR241439	248	12.8	1.5	17	1	CQ617968	ACCESSION:CQ617968
C 176	13.8	1.6	18	1	AX003146	ACCESSION:AX003146	249	12.8	1.5	17	1	CQ617969	ACCESSION:CQ617969
C 177	13.8	1.6	18	1	AX132972	ACCESSION:AX132972	250	12.8	1.5	17	1	CQ622481	ACCESSION:CQ622481
C 178	13.8	1.6	18	1	AX599241	ACCESSION:AX599241	251	12.8	1.5	17	1	CQ622482	ACCESSION:CQ622482
C 179	13.8	1.6	18	1	AX767687	ACCESSION:AX767687	C 252	12.8	1.5	17	1	CQ623027	ACCESSION:CQ623027

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:39:53 ; Search time 3 Seconds
(without alignments)
3.794 Million cell updates/sec

Title: US-10-633-843-3-COPY
Perfect score: 874
Sequence: 1 ctgcagcgtctgggtttcc.....tattaaagaatccaaattc 874

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 363 seqs, 6512 residues

Total number of hits satisfying chosen parameters: 726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 363 summaries

Database : gedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	3.2	28	1	ACCESSION:AR090891
2	28	3.2	28	1	ACCESSION:AR090892
3	28	3.2	28	1	ACCESSION:AR197926
4	28	3.2	28	1	ACCESSION:AR197927
5	28	3.2	28	1	ACCESSION:AR260080
6	28	3.2	28	1	ACCESSION:AR260081
7	27.4	3.1	29	1	ACCESSION:R06744
8	27	3.1	27	1	ACCESSION:AX473368
9	24	2.7	24	1	ACCESSION:AR061116
10	24	2.7	24	1	ACCESSION:AR064690
11	24	2.7	24	1	ACCESSION:AR528355
12	23	2.6	23	1	ACCESSION:AX473370
13	23	2.6	23	1	ACCESSION:AX473371
14	23	2.6	23	1	ACCESSION:AX710079
15	23	2.6	23	1	ACCESSION:AX710080
16	22.6	2.6	30	1	ACCESSION:BD143416
17	22	2.5	29	1	ACCESSION:AR017558
18	21.8	2.5	25	1	ACCESSION:AR064000
19	21.8	2.5	25	1	ACCESSION:AR364465
20	21	2.4	21	1	ACCESSION:BD144206
21	20.4	2.3	22	1	ACCESSION:BD144209
22	20	2.3	21	1	ACCESSION:AR061103
23	20	2.3	21	1	ACCESSION:AR064682
24	20	2.3	21	1	ACCESSION:IO4213
25	20	2.3	21	1	ACCESSION:IO6878
26	20	2.3	21	1	ACCESSION:AR528347
27	19.8	2.3	21	1	ACCESSION:BD174099
28	19	2.2	19	1	ACCESSION:BD144208
29	17.2	2.0	22	1	ACCESSION:A06401
30	17.2	2.0	22	1	ACCESSION:BD172232
31	17.2	2.0	22	1	ACCESSION:BD172551
32	17.2	2.0	22	1	ACCESSION:BD172870
33	17.2	2.0	22	1	ACCESSION:BD173189

C 34	17.2	2.0	22	1	BD175223
C 35	17.2	2.0	22	1	BD260461
C 36	17.2	2.0	22	1	ACCESSION:AR364466
C 37	17.2	2.0	22	1	AR410601
C 38	17.2	2.0	22	1	AR438965
C 39	17.2	2.0	22	1	ACCESSION:AR472985
C 40	17.2	2.0	22	1	ACCESSION:AR526971
C 41	17.2	2.0	22	1	ACCESSION:AR566004
C 42	17.2	2.0	22	1	AX076912
C 43	17.2	2.0	22	1	AX098397
C 44	17.2	2.0	22	1	ACCESSION:AX697416
C 45	17.2	2.0	22	1	BD075372
C 46	17	1.9	17	1	AX671956
C 47	17	1.9	17	1	AX673655
C 48	17	1.9	17	1	AX730213
C 49	17	1.9	17	1	AX733568
C 50	17	1.9	17	1	AX736487
C 51	17	1.9	17	1	AX739220
C 52	17	1.9	17	1	BD174097
C 53	17	1.9	21	1	AR061105
C 54	17	1.9	21	1	AR064684
C 55	17	1.9	21	1	AR528349
C 56	16.8	1.9	20	1	AR338227
C 57	16.8	1.9	21	1	AR061108
C 58	16.8	1.9	21	1	AR064687
C 59	16.8	1.9	21	1	AR528352
C 60	16	1.8	16	1	IO4212
C 61	16	1.8	16	1	IO6877
C 62	16	1.8	17	1	AX081870
C 63	16	1.8	17	1	AX737712
C 64	16	1.8	17	1	AX737721
C 65	16	1.8	18	1	AX378471
C 66	16	1.8	19	1	AR225282
C 67	15.8	1.8	20	1	I73106
C 68	15.8	1.8	20	1	AR305282
C 69	15.8	1.8	20	1	AR309386
C 70	15.8	1.8	20	1	AR350302
C 71	15.8	1.8	21	1	BD061259
C 72	15.8	1.8	21	1	BD061259
C 73	15.6	1.8	17	1	AX707589
C 74	15.6	1.8	17	1	AX707589
C 75	15.4	1.8	17	1	BD255580
C 76	15.4	1.8	17	1	BD255581
C 77	15.4	1.8	17	1	IO6872
C 78	15.2	1.7	20	1	AR121018
C 79	15.2	1.7	20	1	BD272639
C 80	15.2	1.7	20	1	AR0871960
C 81	15.2	1.7	20	1	AR0871961
C 82	15.2	1.7	20	1	AR0871967
C 83	15.2	1.7	20	1	AR0871990
C 84	15.2	1.7	20	1	E27497
C 85	15.2	1.7	20	1	AR531387
C 86	15.2	1.7	20	1	AX167893
C 87	15	1.7	15	1	AR0821402
C 88	15	1.7	15	1	AR0821408
C 89	15	1.7	17	1	AX081871
C 90	15	1.7	17	1	AX706658
C 91	15	1.7	17	1	AX707588
C 92	15	1.7	20	1	AX732679
C 93	15	1.7	20	1	AR199396
C 94	14.8	1.7	19	1	BD195707
C 95	14.8	1.7	19	1	AR282800
C 96	14.8	1.7	19	1	AX129356
C 97	14.4	1.6	17	1	A16196
C 98	14.4	1.6	17	1	A16242
C 99	14.4	1.6	17	1	BD203207
C 100	14.4	1.6	17	1	BD255579
C 101	14.4	1.6	17	1	BD255582
C 102	14.4	1.6	17	1	BD257636
C 103	14.4	1.6	17	1	I23680
C 104	14.4	1.6	17	1	I23682
C 105	14.4	1.6	17	1	AR433547
C 106	14.4	1.6	17	1	AR433549

GenBank/EMBL

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:38:15 ; Search time 0.001 Seconds
(without alignments)
218.500 Million cell updates/sec

Title: US-10-633-843-3-COPY
Perfect score: 874
Sequence: 1 ctgcagcgctcgtgggtttcc.....tattaaagaatccaattc 874

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 125 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 5 summaries

Database : estdb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.4	4.9	48	1	N79542 ACCESSION:N79542
C 2	36	4.1	44	1	H41186 ACCESSION:H41186
C 3	14.8	1.7	19	1	AZ610584 ACCESSION:AZ610584
C 4	11.8	1.4	44	1	H41186 ACCESSION:H41186
C 5	10.8	1.2	14	1	AJ590269 ACCESSION:AJ590269

ALIGNMENTS

RESULT 1
N79542/c
LOCUS N79542 48 bp mRNA linear EST 29-MAR-1996
DEFINITION zb09h12.s1 Soares fetal_lung_NbH119W Homo sapiens cDNA clone IMAGE:301607 3' similar to gb:X02317 SUPEROXIDE DISMUTASE (HUMAN); mRNA sequence.
ACCESSION N79542
VERSION N79542.1 GI:1242243
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 48)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1582
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall: poor quality
Seq primer: m13 -40 forward
High quality sequence stop: 1.

FEATURES

source

1..48
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1246531"
/db_xref="taxon:9606"
/clone="IMAGE:301607"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal lung NbH119W"
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TCGTACCAATCTGAGTGGAGCGCCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbH119W."

Query Match 4.9%; Score 42.4; DB 1; Length 48;
Best Local Similarity 89.6%; Pred. No. 0.18;
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 533 TTCCCTTGATGATGCTGAGGCCCTTAACATCTGTATCTCTCT 580

Db 48 TTCCCTNGGTGTAGTCTGAGGCCCTTACNCATCTGTCTCTCT 1

RESULT 2

H41186
LOCUS H41186 44 bp mRNA linear EST 31-JUL-1995
DEFINITION yN88b11.r1 Soares adult brain N25HB55Y Homo sapiens cDNA clone IMAGE:175485 5' similar to gb:X02317 SUPEROXIDE DISMUTASE (HUMAN); mRNA sequence.

ACCESSION H41186
VERSION H41186.1 GI:917238
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 44)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,B., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1582
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the